

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2001, 13:34:05 ; Search time 57.85 Seconds

(without alignments)
312.059 Million cell updates/sec

Title: US-09-784-340-2

Perfect score: 1 MRSKSLVFLVLLDLPVGC.....KCFIFSCQFKFKTKIEKRE 527

Sequence: 2802

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1732	61.8	530	1	UDBH_HUMAN
2	1729	61.7	528	1	UDBA_HUMAN
3	1713	61.1	530	1	UDBE_HUMAN
4	1712	61.1	528	1	UDBJ_MACFA
5	1691.5	60.4	527	1	UDAL_RAT
6	1686	60.2	530	1	UDBK_MACFA
7	1685	60.1	529	1	UDBI_RAT
8	1676.5	59.8	529	1	UDBT_HUMAN
9	1668.5	59.5	530	1	UDBE_RABIT
10	1661.5	59.3	529	1	UDBG_MACFA
11	1648	58.8	531	1	UDBD_RABIT
12	1635.5	58.4	528	1	UDBA_HUMAN
13	1628.5	58.1	529	1	UDBB_HUMAN
14	1620	57.8	502	1	UDCI_RABIT
15	1595	56.9	530	1	UDBC_RAT
16	1587	56.6	530	1	UDBG_RABIT
17	1580	56.4	530	1	UDBE_RAT
18	1572	56.1	530	1	UDBE_MOUSE
19	1557	55.6	530	1	UDBE_MOUSE
20	1556	55.5	530	1	UDBE_RAT
21	1499	53.5	530	1	UDBE_RAT
22	1137	40.6	533	1	UDBI_HUMAN
23	1128.5	40.3	533	1	UDBI_RAT
24	1124.5	40.1	531	1	UDI5_RAT
25	1122.5	40.1	535	1	UDI1_MOUSE
26	1109	39.6	535	1	UDI1_MOUSE
27	1097.5	39.2	533	1	UDI2_MOUSE
28	1096.5	39.1	530	1	UDI2_HUMAN
29	1094.5	39.1	531	1	UDI3_RAT
30	1092	39.0	531	1	UDI6_MOUSE
31	1081.5	38.6	534	1	UDI3_HUMAN
32	1077	38.4	531	1	UDI6_HUMAN
33	1076.5	38.4	534	1	UDI4_HUMAN

ALIGNMENTS

RESULT	ID	UDBH_HUMAN	STANDARD	PRT	530 AA.
AC	075795				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	UDP-GLUCURONOSYLTRANSFERASE 2B17 PRECURSOR, MICROSOFT (EC 2.4.1.17)				
DE	(UDPCT) (C19-STEROID SPECIFIC UDP-GLUCURONOSYLTRANSFERASE).				
GN	UGT2B17.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Prostate;				
RC	MEDLINE=96394358; PubMed=8798464;				
RA	Beaulieu M., Levesque E., Hum D.W., Belanger A.;				
RT	Isolation and characterization of a novel cDNA encoding a human				
RT	UDP-glucuronosyltransferase active on C19 steroids.";				
RT	J. Biol. Chem. 271:22855-22862(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98030207; PubMed=9364925;				
RA	Beaulieu M., Levesque E., Tchernof A., Beatty B.G., Belanger A.;				
RT	Hum D.W.;				
RT	"Chromosomal localization, structure, and regulation of the UGT2B17				
RT	gene, encoding a C19 steroid metabolizing enzyme.";				
RT	DNA Cell Biol. 16:1143-1154(1997).				
CC	-1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND				
CC	SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND				
CC	ENDOGENOUS COMPOUNDS. THE MAJOR SUBSTRATES OF THIS ISOZYME ARE				
CC	EUGENOL > 4-METHYLMELIFERONE > DIHYDROTESTOSTERONE (DHT) >				
CC	ANDROSTANE-3ALPHA,17BETA-DIOL (3ALPHA-DIOL) > TESTOSTERONE >				
CC	ANDROSTERONE (ADT).				
CC	-1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR				
CC	BETA-D-GLUCURONOSIDE.				
CC	-1- SUBCELLULAR LOCATION: MICROSOFT.				
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES INCLUDING THE				
CC	LIVER, KIDNEY, TESTIS, UTERUS, PLACENTA, MAMMARY GLAND, ADRENAL				
CC	GLAND, SKIN, AND PROSTATE.				
CC	-1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	or send an email to license@isb-sib.ch).				
DR	EMBL: U59209; AAC25491.1; -				
DR	MIM: 601903; -				
DR	InterPro: IPR002213; -				
DR	Pfam: PF00201; UDPGT, 1.				

DR PROSITE: PS00375; UDEPT: 1.
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KM Multigene family; Microsome.
 FT SIGNAL 1 23
 FT CHAIN 24 530
 FT TRANSMEM 495 515
 FT CARBOHYD 65 65
 FT CARBOHYD 316 316
 FT CARBOHYD 483 483
 SQ SEQUENCE 530 AA; 61095 MW; 8E59EB043CF43760 CRC64;

Query Match
 Best Local Similarity 61.8%; Score 1732; DB 1; Length 530;
 Matches 326; Conservative 74; Mismatches 112; Indels 18; Gaps 3;

9 VELLQLQFC-VGCGFGKGLVWPCMSHWLANKVILEELIVGHEVTVLTHSKPSLIDYR 67
 8 VELLQLQFCVSSGCGKGLVWPCMSHWLANKVILEELIVGHEVTVLTHSKPSLIDYR 67
 68 KPSAKFEVYHMPDRTENELEIFVDLAINVLPGLSTWOSVILNDFEYIRCTLMK- 123
 68 KSSAKILEVYPTSLTKNLEDEFFMK- - - - -FDRWYISISKNTFWVSFSLQELCMEY 120
 124 - - - - -KCESFTYNOTLKKKLOETNYDMLIDPVIPCGDIAELLAVPPVLTIRISVGN 177
 121 SDYNIKICEADVANKKMKRKQESKFDVLLADAVNPGCELLAELLNIPFLYSIRFVGYT 180
 178 MERSCGKIPAEVSVVPVMTGLTRMPLERKNSMLSVLFHFVIOVDYHWFEEFYKA 237
 181 VEKNGGGLFPSPVYVPMSELSDQMEIKMNTYLYLDFDFQAVDLKKMDFSEV 240
 238 LGRTTTCETVYGAEMIRTPYMPPEPPPOYPPEVYGGIHCCKPAKALPKEMENVOSS 297
 241 LGRTTTEFTMGKEMMLIRTPYMPPEPPPOYPPEVYGGIHCCKPAKALPKEMENVOSS 300
 298 GEDGIVFSGSGFQNTYEEKANIASALAOIPQKVLRYKGGKPSLGNATRIYDIPQ 357
 301 GENGIYVFSGSMISNSESANMIASALAOIPQKVLRYKGGKPSLGNATRIYDIPQ 360
 358 NDLLGHKTKAFTHGMCNIGYFAIYHGVPMGVPIFGDLDNIAHKAAGAIVEINFT 417
 361 NDLLGHKTKAFTHGMCNIGYFAIYHGVPMGVPIFGDLDNIAHKAAGAIVEINFT 420
 418 MISEDLLRALRYITDSSYKEMARLSRIHHDPVKPLDAVWIEFVMMHKAHKAHLSA 477
 421 MSSRDLLNALKSVINDPYKENIMKLSRIHHDPVKPLDAVWIEFVMMHKAHKAHLSA 480
 478 AHDLTWFQHSIDVIGFLTCVATAIPLFTKCFLESCQKFNKTRIEKRE 527
 481 AHDLTWFQHSIDVIGFLTCVATAIPLFTKCFLESCQKFNKTRIEKRE 530

RESULT 2
 UDB4_HUMAN STANDARD. PRT: 528 AA.
 AC P06133; P36538; O60731; O60867;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
 DE (UDEPT) (HYDROXYCHOLIC ACID) (HLDG25) (UDEPTH-1).
 GN UGT2B4 OR UGT2B11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-87241362; PubMed-3109396;
 RA Jackson M.R., McCarthy L.R., Harding D., Wilson S., Coughtrie M.W.H.,
 Burchell B.;

RT "Cloning of a human liver microsomal UDP-glucuronosyltransferase
 RT cDNA.";
 RL Biochem. J. 242:581-588(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-93326164; PubMed-8333863;
 RA Jin C.-Y., Miners J.O., Lillywhite K.J., McKenzie P.I.;
 RT "cDNA cloning and expression of two new members of the human liver
 RT UDP-glucuronosyltransferase 2B subfamily.";
 RL Biochem. Biophys. Res. Commun. 194:496-503(1993).
 RN [3]
 RP SEQUENCE FROM N.A. AND VARIANT GLU-458.
 RA Levesque E., Beaulieu M., Belanger A.;
 RT UGT2B4(E458): a UDP-glucuronosyltransferase encoded by a polymorphic
 RT gene with differential substrate specificity.";
 RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: UDEPT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS. ACTIVE ON POLYHYDROXYLATED ESTROGENS (SUCH
 CC AS ESTRADIOL, 4-HYDROXYESTRONE AND 2-HYDROXYESTRADIOL) AND XENOBIOTICS
 CC (SUCH AS 4-METHYLBELIFERONE, 1-NAPHTHOL, 4-NITROPHENOL,
 CC 2-AMINOPHENOL, 4-HYDROXYBIPHENYL AND MENTHOL).
 CC -1- FUNCTION: CAPABLE OF 6 ALPHA-HYDROXYGLUCURONIDATION OF
 CC HYDROXYCHOLIC ACID.
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCURONOSIDE.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
 CC CAUTION: REF.2 THOUGHT THAT THIS WAS A NEW FORM (UGT2B11). THE
 CC NAME UGT2B11 HAS NOW BEEN REUSED FOR ANOTHER HUMAN ENZYME.
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 CC EMBL: Y00317; CA68415.1; -
 CC EMBL: AF064200; AAC95002.1; -
 CC EMBL: AJ005162; CA06396.1; -
 CC PIR: A27878; A27878.
 CC PIR: J06019; J06019.
 CC MIM: 600067; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDEPT: 1.
 DR PROSITE: PS00375; UDEPT: 1.
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KM Multigene family; Microsome; Polymorphism.
 FT SIGNAL 1 23
 FT CHAIN 24 528
 FT TRANSMEM 493 509
 FT CARBOHYD 315 315
 FT VARIANT 458 458
 FT FT
 FT CONFLICT 109 109
 FT CONFLICT 171 172
 FT CONFLICT 382 387
 FT CONFLICT 396 396
 SQ SEQUENCE 528 AA; 60512 MW; 6B45E6769971A078 CRC64;

Query Match
 Best Local Similarity 61.7%; Score 1729; DB 1; Length 528;
 Matches 332; Conservative 61; Mismatches 131; Indels 4; Gaps 3;

Qy 3 SDKSAVFLLIQLQFC-VGCGFGKGLVWPCMSHWLANKVILEELIVGHEVTVLTHSKP 61
 Db 2 SMKTSALLLIQLQFCVSSGCGKGLVWPCMSHWLANKVILEELIVGHEVTVLTHSKP 61
 Qy 62 SLIDYRRPSALKFEVYHMPDRTENELEIFVDLAIN-VLPGLSTWOSVILNDFEYIRG 119

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Db 62 ISFDNSSTLTFEYVPSLTTEEDITKOLVKRAELPKTFMSYSOQVEIMTFEND 121
Qy 120 TLKMCESFYNOTLMMKLOETNYDVMIDIPYPCGDLMAELAVFVTLTRISVGNNM 179
Db 122 ILRKCKDVISKMLKMLKQESRFDVLAADVFPFGLLAEELKIPFYVSLRSPYALE 181
Qy 180 RSCGLPAPLSTYVPMGIDVDRMTFLERVKNSMLSVLFHEFIODYHFWEFYSKALG 239
Db 182 KHSGLLEPPSPVPVPMSELSDQMFEIERVKMIYVLFEEFQIFDMKMOQFYSEVIG 241
Qy 240 RPTTCEVNGKAELIIRYPMDFEPOPQOPNFEVGGHCHCAKAPALPKEMENFYOSSGE 299
Db 242 RPTTSEMAKADIMLIRYPMDFEPOPQOPNFEVGGHCHCAKAPALPKEMENFYOSSGE 301
Qy 300 DGIVFSLGSLFQNTYEKANIIASALAQIPQVLMRYKGRKSTLGANTRLYDWIPOND 359
Db 302 NGVVFSLGSMVSNSEERANYIASLAKIPQVLMRFEGNKPDLGLNTRLYKWIPOND 361
Qy 360 LIGHKTAFTHGKNGIYEALYICGVPMVGPPIFGDOLDNIAHMKAKAAVEINEFKMT 419
Db 362 LIGHKTAFTHGKNGIYEALYICGVPMVGPPIFGDOLDNIAHMKAKAAVSLDFHTMS 421
Qy 420 SEDLLRALRTVTDSSYKENAMRLSRTHHDOPVKPLDRAVFNIEFMRHKGAKHLRSAH 479
Db 422 STDLLNALRTVTDSSYKENAMRLSRTHHDOPVKPLDRAVFNIEFMRHKGAKHLRVAH 481
Qy 480 DLTWFOHYSIDVIGFLTCVATAIFLTKCFELFSCQENKTRIEKRE 527
Db 482 DLTWFOHYSIDVIGFLTCVATAIFLTKCFELFSCQENKTRIEKRE 528

RESULT 3
IDBDF_HUMAN STANDARD: PRT; 530 AA.
AC P54855; P23765; Q9UK63;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE UDP-GLUCUCURONOSYLTRANSFERASE 2B15 PRECURSOR, MICROSMAL (EC 2.4.1.17)
DE (UDPGLT) (UDPGRH-3) (HLUG4).
GN UGT2B15 OR UGT2B8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95136867; PubMed=7835232;
RA Green M.D., Oturu E.M., Tepfly T.R.;
RA "Stable expression of a human liver UDP-glucuronosyltransferase
RT (UGT2B15) with activity toward steroid and xenobiotic substrates.";
RL Drug Metab. Dispos. 22:799-805(1994).
RN [2]
RP SEQUENCE OF 8-530 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90343358; PubMed=2116769;
RA Coffman B.L., Tepfly T.R., Irishaid Y.M., Green M.D., Smith C.,
RA Jackson M.R., Wooster R., Burchell B.;
RA "Characterization and primary sequence of a human hepatic microsomal
RT estriol UDPglucuronosyltransferase.";
RL Arch. Biochem. Biophys. 281:170-175(1990).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT TYR-85.
RX MEDLINE=97439504; PubMed=9295060;
RA Levesque E., Beaulieu M., Green M.D., Tepfly T.R., Belanger A.,
RA Hum D.W.;
RA "Isolation and characterization of UGT2B15(Y85): a
RT UDP-glucuronosyltransferase encoded by a polymorphic gene.";
RL Pharmacogenetics 7:317-325(1997).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

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CC ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD
CC SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES, INCLUDING SIMPLE
CC PHENOLIC COMPOUNDS, 7-HYDROXYLATED COUMARINS, FLAVONOIDS,
CC ANTHRAQUINONES, AND CERTAIN DRUGS AND THEIR HYDROXYLATED
CC METABOLITES. IT ALSO CATALYZES THE GLUCURONIDATION OF ENDOGENOUS
CC STEROIDS AND ANDROGENS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC -1- SUBCELLULAR LOCATION: MICROSMAL.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -1- CAUTION: REF.2 THOUGHT THAT THIS WAS A SEPARATE FORM (UGT2B8). THE
CC NAME UGT2B8 HAS NOW BEEN REUSED FOR A RAT ENZYME.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: U08854; AAC50077.1; -.
CC EMBL: U06641; AA83406.1; -.
CC EMBL: AF180322; AAD55093.1; -.
CC PIR: S11309; S11309.
CC DR MIM: 600069; -.
CC DR InterPro: IPR002213; -.
CC DR Pfam: PF00201; UDPGT. 1.
CC DR PROSITE: PS00375; UDPGT. 1.
CC KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC Multigene family; Microsome; Polymorphism.
CC FT SIGNAL 1 23
CC FT CHAIN 24 530
CC FT TRANSMEM 495 515
CC FT CARBOHYD 65 65
CC FT CARBOHYD 316 316
CC FT CARBOHYD 483 483
CC FT VARIANT 85 85
CC FT FTID-VAR_007713.
CC FT CONFLICT 119 119 E -> A (IN REF. 2).
CC FT CONFLICT 145 145 K -> R (IN REF. 2).
CC FT CONFLICT 150 155 LADALN -> PGDPVF (IN REF. 2).
CC FT CONFLICT 162 162 A -> S (IN REF. 2).
CC FT CONFLICT 165 165 F -> L (IN REF. 2).
CC FT CONFLICT 170 177 LYSRFSV -> VYRSRIS (IN REF. 2).
CC FT CONFLICT 181 181 F -> I (IN REF. 2).
CC FT CONFLICT 203 203 S -> I (IN REF. 2).
CC FT CONFLICT 293 293 M -> L (IN REF. 2).
CC FT CONFLICT 401 401 H -> D (IN REF. 2).
CC FT CONFLICT 443 443 V -> A (IN REF. 2).
CC FT CONFLICT 501 501 C -> W (IN REF. 2).
CC FT CONFLICT 523 523 T -> K (IN REF. 2).
CC SEQUENCE 530 AA; 60961 MW; 23DDA4B99687ECB4 CRC64;

Query Match 61.1%; Score 1713; DB 1; Length 530;
Best Local Similarity 62.0%; Pred. No. 1,le-127;
Matches 327; Conservative 74; Mismatches 114; Indels 12; Gaps 5;
Qy 9 VFLLDLPFC-VGCGFGKYLWPCDMSHMLNVAVILBELIRGHEVTVLTHKPSLIDR 67
Db 8 VFLLDLPFCVSSGSCGKYLWPCDSHMLNVAVILBELIRGHEVTVLTHKPSLIDR 67
Qy 68 KPSALKEFVHPMDRTEENELFVDALNVLPR---GLST---QSVIKLNDFEVETR 120
Db 68 KPSALKEFVHPMDRTEENELFVDALNVLPR---GLST---QSVIKLNDFEVETR 123
Qy 121 LKMCESFYNOTLMMKLOETNYDVMIDIPYPCGDLMAELAVFVTLTRISVGNNM 180
Db 124 SKKCKDAVNLKMLKMLKQESRFDVLAADVFPFGLLAEELKIPFYVSLRSPYALE 183
Qy 181 SCGKLPAPLSTYVPMGIDVDRMTFLERVKNSMLSVLFHEFIODYHFWEFYSKALG 240

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DB 184 NGCGLEFPSPYVWVMSLSDQMIMERKKNMIMHIEPWFQIYDLKMDQFYSVIGR 243
 QY 241 PTTLETVGKATINLIRTYWDEFPPOYPONFEVGGHCHCPAKALPKEMENVOSSGED 300
 DB 244 PTTLETVGKATINLIRTYWDEFPPOYPONFEVGGHCHCPAKALPKEMENVOSSGED 303
 QY 301 GIVFSLGSPONTVEERKANITASALAOIPKVLRYKRGKSTGANTRLTYDLPOND 360
 DB 304 GIVFSLGSPONTVEERKANITASALAOIPKVLRYKRGKSTGANTRLTYDLPOND 363
 QY 361 LGHPTKAFITHGNGNGIYEAIGHGVNVPVPIEGDQDNTAHMKAGAAVEINFKTMTS 420
 DB 364 LGHPTKAFITHGNGNGIYEAIGHGVNVPVPIEGDQDNTAHMKAGAAVEINFKTMTS 423
 QY 421 EDLRLATFTVTDSSYKKNMARLSRIHHDDPVKPLDRAVNIETVYMRHKGAKHLRSAAD 480
 DB 424 RDLNALKSVINDYVYKKNMARLSRIHHDDPVKPLDRAVNIETVYMRHKGAKHLRSAAD 483
 QY 481 LTMFOHYSIDVIGFLTCVATAIFLFTKCFLEFSCOKENKTRKIEKRE 527
 DB 484 LTMFOHYSIDVIGFLTCVATAIFLFTKCFLEFSCOKENKTRKIEKRE 530

RESULT 4
 DBL MACFA STANDARD; PRT; 528 AA.

AC 09XT55; 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 GN UDP-GLUCURONOSYLTRANSFERASE 2B19 PRECURSOR, MICROSOMAL (EC 2.4.1.17).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_TaxID=9541;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Liver, and Prostate;
 RC MEDLINE=99203465; PubMed=10102998;
 RA Belanger G., Barbier O., Hum D.W., Belanger A.;
 RT Molecular cloning, expression and characterization of a monkey
 RT steroid UDP-glucuronosyltransferase, UGT2B19, that conjugates
 RT testosterone *;
 RL Eur. J. Biochem. 260:701-708(1999).
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD
 CC SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES: EUGENOL, 4-
 CC METHYLBELLOLIPERONE, P-NITROPHENOL, 1-NAPHTHOL, P,P'-BIPHENOL,
 CC MARINEENIN AND O,O'-BIPHENOL. ACTIVE ALSO ON 3A-HYDROXY AND 17B-
 CC HYDROXY POSITIONS OF STEROIDS.
 CC -1- FUNCTION: CONTRIBUTES TO THE FORMATION OF ANDROGEN GLUCURONIDE IN
 CC EXTRAHEPATIC STEROID TARGET TISSUES SUCH AS THE PROSTATE.
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCORONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCORONOSIDE.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, OVARY, PROSTATE, COLON,
 CC KIDNEY, PANCREAS, BRAIN, CEREBELLUM, MAMMARY GLAND AND EPIDIDYMIS.
 CC NOT EXPRESSED IN SMALL INTESTINE, SPLEEN, BLADDER, ADRENAL GLAND
 CC AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.

DR EMBL: AF112112; AAD24435.1; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UPGT. 1.
 DR PROSITE: PS00375; UPGT. 1.
 KM Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KM Multigene family; Microsome.
 FT SIGNAL 1; 21
 FT CHAIN 22 528
 FT TRANSMEM 493 513
 FT CARBOHYD 315 315
 SO SEQUENCE 528 AA; 60741 MW; 3BFD2AE714A27AEE CRC64; POTENTIAL.
 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 61.1%; Score 1712; DB 1; Length 528;
 Best Local Similarity 61.8%; Pred. No. 1.3e-127;
 Matches 329; Conservative 65; Mismatches 126; Indels 12; Gaps 5;

QY 3 SDKSAVFLILQIFC-VGCGFCGVLVNPMCDMSHMLNVKYLIELIVRGHEVLTSHKP 61
 DB 2 SMKWTSAALLILQISCYLFSFGCGVLVNPMCDMSHMLNVKYLIELIVRGHEVLTSHKP 61
 QY 62 SLIDYRRPSALKEFVHMPDQRTENEIPVDLALNVPGLST-----WQSVKLNDFV 115
 DB 62 ILDPNNPSPLEKEI--CPTSITET--FQDSYQVLRKMSDKRQTFWPHFLHVOEMM 117
 QY 116 EIRGTLKMCESFIYNOTLKKIQTNYDVLIDPVIPCGDLMAELLAVPVLTRISVG 175
 DB 118 TYGDMIRKFCQDVVSNKMLKKIQLQESRFVDVLAIDAPSCGELLAEIKIFVYSLRSPG 177
 QY 176 GNNERSGCRIPAPLSYVPMVMTGLDRMTLEVKNSMLSVLHFVLTQDYHFWEEFYS 235
 DB 178 YALEKHGGFLFPSPYVPMVMTGLDRMTLEVKNSMLSVLHFVLTQDYHFWEEFYS 237
 QY 236 KALGPTTLCETVGAKEIWLIRTYWDEFPPOYPONFEVGGHCHCPAKALPKEMENVO 295
 DB 238 KYLGRPTTLEIEMAKAEIWLIRTYWDEFPPOYPONFEVGGHCHCPAKALPKEMENVO 297
 QY 296 SSGEDGIVFSLGSPONTVEERKANITASALAOIPKVLRYKRGKSTGANTRLTYD 355
 DB 298 SSGDNVYVFSLSQSVNSSEERANITASALAOIPKVLRYKRGKSTGANTRLTYD 357
 QY 356 PONDLLGHKPTKAFITHGNGNGIYEAIGHGVNVPVPIEGDQDNTAHMKAGAAVEINF 415
 DB 358 PONDLLGHKPTKAFITHGNGNGIYEAIGHGVNVPVPIEGDQDNTAHMKAGAAVEINF 417
 QY 416 KMTSFDLRLATFTVTDSSYKKNMARLSRIHHDDPVKPLDRAVNIETVYMRHKGAKHL 475
 DB 418 DTMSTDLNALKTVINDYVYKKNMARLSRIHHDDPVKPLDRAVNIETVYMRHKGAKHL 477
 QY 476 SAADLTMFOHYSIDVIGFLTCVATAIFLFTKCFLEFSCOKENKTRKIEKRE 527
 DB 478 VAADLTMFOHYSIDVIGFLTCVATAIFLFTKCFLEFSCOKENKTRKIEKRE 528

RESULT 5
 UDAL_RAT STANDARD; PRT; 527 AA.

AC P36510; 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 01-JUN-1994 (Rel. 29, Last annotation update)
 GN UDP-GLUCURONOSYLTRANSFERASE 2A1 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91156050; PubMed=1900353;
 RA Lazard D., Zupko K., Poria Y., Nef P., Lazarovits J., Horn S.,
 Khen M., Lancelot D.;

RT "Odorant signal termination by olfactory UDP glucuronosyl
RT transferase.":
CC Nature 349:790-793(1991).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS. THIS ISOFORM IS ACTIVE ON OROARATS AND
CC SEEMS TO BE INVOLVED IN OLFACTION. IT COULD HELP CLEAR LIPOPHILIC
CC OROARAT MOLECULES FROM THE SENSORY EPITHELIUM.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCORONOSIDE.
CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X57565; -; NOT_ANNOTATED_CDS.
CC InterPro: IPR002213; -;
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC DR Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC KM Multigene family; Microsome; Olfaction.
CC FT SIGNAL 1 20
CC FT CHAIN 21 527 UDP-GLUCURONOSYLTRANSFERASE 2A1.
CC FT TRANSMEM 491 507 POTENTIAL.
CC FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 527 AA; 59915 MW; 6A32A9B56E8BDE CRC64;

Query Match 60.4%; Score 1691.5; DB 1; Length 527;
Best Local Similarity 61.5%; Pred. No. 5.3e-126;
Matches 324; Conservative 69; Mismatches 113; Indels 21; Gaps 5;

OY 13 LQLFCVCGFCGKRVLPDCDSHMLNWKVLEELVGRHEVTVLTHSKPSLIDYRRPSAL 72
DB 10 LQLSLGMSLGVNLVLPMEGSHMLNWKVLEELVGRHEVTVLTHSKPSLIDYRRPSAL 69
OY 73 KEVYVAMPDRRENEIFDIALNLV---PGLSTWQSVLK-----LNDFFVEIRGLTKMM 124
DB 70 TEIYVPPVPGKKEIESVIVDFVLTWLENRPSSTIWTFKENAKVIEEFLVSRG----I 125
OY 125 CSSEFYNNFLMKLOETNTDVMVLDVIPCGLMALLAVPVLTLRISVGMERSCK 184
DB 126 CGGVNLNENKMLRKLGRKEVLLSDPFGDVALKLGIPFLYSLSFSPASTVERKCGK 185
OY 185 LPAPLSYVVPMTGLDRMTFLERKNSMLSVLFHFMDYDYHF---WEEFYSKALGR 240
DB 186 VEPPEYVVAIISELFLDQMSFADRVN----FISYRMQDMYETLMKQMSDYSSALGR 240
OY 241 PPTLCTEYVKAETIWLIRIYWDPEEPQYQPNNEEFVGGHCKPAKALPKEMENFVSSGED 300
DB 241 PPTLCTEYVKAETIWLIRIYWDPEEPQYQPNNEEFVGGHCKPAKALPKEMENFVSSGED 300
OY 241 PPTLCTEYVKAETIWLIRIYWDPEEPQYQPNNEEFVGGHCKPAKALPKEMENFVSSGED 300
DB 241 PPTLCTEYVKAETIWLIRIYWDPEEPQYQPNNEEFVGGHCKPAKALPKEMENFVSSGED 300
OY 301 GIVNPSISGLFQNVMEKANIATASALAQIPQVLYMKYKGGKPSSTLCANRLYIMIQNDL 360
DB 301 GIVNPSISGLFQNVMEKANIATASALAQIPQVLYMKYKGGKPSSTLCANRLYIMIQNDL 360
OY 361 LGHPKRAITITGNGMNGIEATYHGVPMGVPIFGDQDNLIAHMKAGAVEINFRTMTS 420
DB 361 LGHPKRAITITGNGMNGIEATYHGVPMGVPIFGDQDNLIAHMKAGAVEINFRTMTS 420
OY 421 EDLLRALRTVITDSSYKENAMRLSRTHDQPVKPLDRAVFWIEFVNRHKGAKHLRSAAHD 480
DB 421 EDLLRALRTVITDSSYKENAMRLSRTHDQPVKPLDRAVFWIEFVNRHKGAKHLRSAAHD 480
OY 481 LWFQHYSDIVGELLTCAVATAFLETKCFPLSCQKFNTRKIERKE 527
DB 481 LWFQHYSDIVGELLTCAVATAFLETKCFPLSCQKFNTRKIERKE 527

DB 481 LWFQHYSDIVGELLTCAVATAFLETKCFPLSCQKFNTRKIERKE 527

RESULT 6
ID UDBK MACFA STANDARD; PRT; 530 AA.
AC 077649;
DT 15-DEC-1998 (rel. 37, Created)
DT 15-DEC-1998 (rel. 37, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B20 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DN (UDPCT).
OS UGT2B20.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and prostate;
RA Barbier O., Belanger A., Hum D.W.;
RT "Cloning and characterization of a simian UDP-glucuronosyltransferase
RT enzyme, UGT2B20, a novel steroid conjugating protein.";
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCORONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF072223; AAD08808.1; -;
CC InterPro: IPR002213; -;
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC DR Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC KM Multigene family; Microsome.
CC FT SIGNAL 1 23
CC FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B20.
CC FT TRANSMEM 495 515 POTENTIAL.
CC FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 530 AA; 61225 MW; A5EB47F8D517DBDA CRC64;

Query Match 60.2%; Score 1686; DB 1; Length 530;
Best Local Similarity 60.7%; Pred. No. 1.5e-125;
Matches 321; Conservative 76; Mismatches 112; Indels 20; Gaps 5;

OY 9 VFLLDLFC-VGCGFCGKRVLPDCDSHMLNWKVLEELVGRHEVTVLTHSKPSLIDR 67
DB 8 VFLLDLFCVSSGSGCKRVLPDCDSHMLNWKVLEELVGRHEVTVLTHSKPSLIDR 67
OY 68 KPSALKEVYVAMPQDTEENEIFVDLNLVPLGLSTWQSVLKLNDFVEIRGLTKMMCS 127
DB 68 KPSALKEVYVAMPQDTEENEIFVDLNLVPLGLSTWQSVLKLNDFVEIRGLTKMMCS 127
OY 128 FIV-----NOTLKKKLOETNYDVALDVIPICGDLMAELLAVPVLTLRISVSG 176
DB 120 YYYSSKICKDANVLNKKMLTKLTKETKFDVILADALNPGCGELLAELNIPVYSLRFTVG 179

OX NCBI_TaxId=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90243659; PubMed=2159463;
RA Rittler J.K., Sheen Y.Y., Owens I.S.;
RT "Cloning and expression of human liver UDP-glucuronosyltransferase in COS-1 cells, 3,4-catechol estrogens and estrinol as primary substrates.";
RT J. Biol. Chem. 265:7900-7906(1990).
RL
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.
CC -1- FUNCTION: ITS UNIQUE SPECIFICITY FOR 3,4-CATECHOL ESTROGENS AND ESTRIOL SUGGESTS IT MAY PLAY AN IMPORTANT ROLE IN REGULATING THE LEVEL AND ACTIVITY OF THESE POTENT AND ACTIVE ESTROGEN METABOLITES.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC
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CC
CC EMBL: J05428; AAA36793.1; -
CC PIR: A35366; A35366.
DR MIM: 600068;
DR InterPro: IPR00213; -
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KM Transferase: Glycosyltransferase; glycoprotein; Transmembrane; Signal;
KM Multigene family; Microsome.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 529 UDP-GLUCURONOSYLTRANSFERASE 2B7.
FT TRANSMEM 493 509 POTENTIAL.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 529 AA; 60694 MW; 94B1CACE92F146 CRC64;

Query Match 59.8%; Score 1676.5; DB 1; Length 529;
Best Local Similarity 60.6%; Pred. No. 8,2e-125;
Matches 320; Conservative 67; Mismatches 138; Indels 3; Gaps 3;

DB 302 NGVVFSLGSWNSNMTEERANVIASALAOIPQKVLNRFDPGKPKPTLGLNRLYKWIPOND 361
QY 360 LGGPKTKAFRTTHGNGMCIETATYHGVPMGVPIFGOLDNIAMKRGAAVEINFTMT 419
DB 362 LGGPKTKAFRTTHGANGIETATYHGVPMGVPIFGOLDNIAMKRGAAVEINFTMTS 421
QY 420 SEDLLRLRLRYTTFSSYKEMAMRLSRIRHDDQVPFLDRAVWIEFWNRHKGAKHLRSAAH 479
DB 422 STDLLNKLKRYINDPSTKENYMKLSRIHQDPKVPFLDRAVWIEFWNRHKGAKHLRVAAH 481
QY 480 DLTFWFOYSIDVIGFLTCVATAFLFTKCFLESCOFENRTKIEKRE 527
DB 482 DLTFWFOYSIDVIGFLTCVATAFLFTKCFLESCOFENRTKIEKRE 529

RESULT 9
ID DBE_RABIT STANDARD; PRT; 530 AA.
AC P36513;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B14 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (EGT12).
GN UGT2B14.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;
RX MEDLINE=93315511; PubMed=8325897;
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tepfly T.R.;
RT "Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.";
RT J. Biol. Chem. 268:15260-15266(1993).
RL
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBITS.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC
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CC
CC EMBL: L01082; AAA18021.1; -
CC PIR: C47113; C47113.
DR InterPro: IPR00213; -
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KM Transferase: Glycosyltransferase; glycoprotein; Transmembrane; Signal;
KM Multigene family; Microsome.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 530 UDP-GLUCURONOSYLTRANSFERASE 2B14.
FT TRANSMEM 494 510 POTENTIAL.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 530 AA; 60664 MW; CEA44BF25B53CB35 CRC64;

Query Match 59.5%; Score 1668.5; DB 1; Length 530;
Best Local Similarity 58.2%; Pred. No. 3,5e-124;
Matches 310; Conservative 86; Mismatches 116; Indels 21; Gaps 4;

QY 7 ALVFLLLDFCVGC---GPGCKVLYWPCDMSHMLNVKYLEELIVRGHEVTLTHSKSL 63
 Db 7 SVLLLLDLQSC--CPRGSCGVLYWPCDMSHMLNVKYLEELIVRGHEVTLTHSKSL 64
 QY 64 IDYRPSALKFEVYMPDPRTEENEIYVDLNLVPGSLTWSVYK-----LNDPE 114
 Db 65 IDPSKQAMIKETEPPIATKDLLEDFVHY-----YSTWNAQNSQWKFSLQKLF 117
 QY 115 VEIRGTLKMGESFYNTLTKKLOETNYDVLIDPVIIPCGDLMAELLAVPVTLRISV 174
 Db 118 SEYSDSCNACKEVYFNKTLTKLOESRFDLLSDAIPCEGLLAELLKIPFVSLRPTP 177
 QY 175 GGNMRSCKGLPAPLSYVPVMTGLTDMRTEFLERYKNSMLSVLFHFVIQDYDHFHEEY 234
 Db 178 GYTMKYSKGLSPVSPYPIILSDLSGKMTMERNMNLMLYDFEWMQNRKRWDFY 237
 QY 235 SKALGRPTLCEYTGKAEIWLIRTYWDFEPOPOPNFEVGLHCKPAKALPREMENFV 294
 Db 238 SEVIGRPVTSSELVKGADMLIRSYWDLFEPRPLPNIOFGVGLHCKPAKALPREMEFV 297
 QY 295 QSGEDGIVVFSGLSPONTTEERKANIISALAOIPKVLIRYKGGKPRSTGANTRLYDW 354
 Db 298 QSSGEVGVVFSGLSMTNMEERANLISAFADLPKQVIRFGQKPEYLGPMTRLYDW 357
 QY 355 IPONDLLGHKRTAFITHGNGIYEALYHGVWGVPIEGDOLDNTAHMKAGAWEIN 414
 Db 358 IPONDLLGHKRTAFITHGNGIYEALYHGVWGVPIEGDOLDNTAHMKAGAWEIN 417
 QY 415 EKTWTSDDLRLALRTVYTDSSYKENAMRLSIHDDPVKPLDRAVFIIEVYMRKGAHL 474
 Db 418 WKTWTSDDLRLALRTVYTDSSYKENAMRLSIHDDPVKPLDRAVFIIEVYMRKGAHL 477
 QY 475 RSAHDLTFMFOHYSIDVIGFLTCVATAIPLFKCFLFSCQKFKTRIKRE 527
 Db 478 RVAHDLTFMFOHYSIDVIGFLTCVATAIPLFKCFLFSCQKFKTRIKRE 530
 RESULT 10
 UDB8_MACFA STANDARD; PRT; 529 AA.
 AC 002663;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE UDP-GLUCURONOSYLTRANSFERASE 289 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
 GN UG1289.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=98030212; PubMed=9364930;
 RA Belanger G., Beaulieu M., Levesque E., Hum D.W., Belanger A.:
 RT "Expression and characterization of a novel
 RT UDP-glucuronosyltransferase, UGT2B9, from cynomolgus monkey."
 RL DNA Cell Biol. 16:1195-1205(1997).
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS. THIS ISOZYME IS ACTIVE ON C18, C19, AND C21
 CC STEROIDS, BILE ACIDS, AND SEVERAL XENOBIOTICS INCLUDING EUGENOL,
 CC 1-NAPHTHOL, AND P-NITROPHENOL.
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCURONOSIDE.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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 CC
 DR EMBL: U91582; AB050249.1;
 DR InterPro: IPR002213;
 DR Pfam: PF00201; UDPGT. 1.
 DR PROSITE: PS00375; UDPGT. 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome.
 FT SIGNAL 1 ?
 FT CHAIN 1 529
 FT TRANSMEM 494 514
 FT CARBOHYD 67 67
 FT CARBOHYD 68 68
 FT CARBOHYD 88 88
 SQ SEQUENCE 529 AA; 60970 MW; F110F85FE3A9DBBD CRC64;
 Query Match 59.3%; Score 1661.5; DB 1; Length 529;
 Best Local Similarity 60.2%; Pred. No. 12e-123;
 Matches 320; Conservative 65; Mismatches 136; Indels 11; Gaps 3;
 QY 3 SDRKALVFLLIQ-FCYGCFCGVLYWPCDMSHMLNVKYLEELIVRGHEVTLTHSKP 61
 Db 2 SVKWTSVILLIQLSYSSSCGVLYWMAEYSHMMNKLTLEELVYRGHEVTLTHSKSAS 61
 QY 62 SLIDYRPSALKFEVYMPDPRTEENEIYVDLNLVPGSLTWSVYKLNDFPV 115
 Db 62 ILFDPNNSALKIEVFTSLTKTE---FENISQEKRIELPKDFWLYFSQMOETIMW 117
 QY 116 EITGTLKMGESFYNTLTKKLOETNYDVLIDPVIIPCGDLMAELLAVPVTLRISV 175
 Db 118 RFQDIIIRNPKCDVYVSNKMKKLOESRFDVADPILPCSELLAEELNIPVLSRPTP 177
 QY 176 GGNMRSCKGLPAPLSYVPVMTGLTDMRTEFLERYKNSMLSVLFHFVIQDYDHFHEEY 235
 Db 178 YIFKHCQGLFPSPSYVPMVSELSDQMTMERKNITWLSDFYFQWDMKRWDFYS 237
 QY 236 KALGRPTLCEYTGKAEIWLIRTYWDFEPOPOPNFEVGLHCKPAKALPREMENFV 295
 Db 238 EYVGRPTLSETGWKADIMLIRSNWNPQPHPLPVDFVGLHCKPAKALPREMEFV 297
 QY 296 SSGEDGIVVFSGLSPONTTEERKANIISALAOIPKVLIRYKGGKPRSTGANTRLYDW 355
 Db 298 SSGENGVVFSGLSMTNMEERANVIALAOIPKVLIRFGKRPDTGLNTRLYKWI 357
 QY 355 PONDLLGHKRTAFITHGNGIYEALYHGVWGVPIEGDOLDNTAHMKAGAWEIN 415
 Db 358 PONDLLGHKRTAFITHGNGIYEALYHGVWGVPIEGDOLDNTAHMKAGAWEIN 417
 QY 416 KTWTSDDLRLALRTVYTDSSYKENAMRLSIHDDPVKPLDRAVFIIEVYMRKGAHL 475
 Db 418 DTMSTDLANRLKTYINDLYKENWKLIRIHDQPVKPLDRAVFIIEVYMRKGAHL 477
 QY 476 SAHDLTFMFOHYSIDVIGFLTCVATAIPLFKCFLFSCQKFKTRIKRE 527
 Db 478 RAHDLTFMFOHYSIDVIGFLTCVATAIPLFKCFLFSCQKFKTRIKRE 529
 RESULT 11
 UDBD_RABIT STANDARD; PRT; 531 AA.
 AC P36512;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 2B13 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
 DE (UDPgt) (EGT10).
 GN UGT2B13.
 OS Oryctolagus cuniculus (Rabbit).

Query Match	Score 1635.5; DB 1; Length 528;
Query Local Similarity	59.8%; Pred. No. 1,4e-121;
DB	SSGEGVVVFSIGSINSLTEERANVASALAOLPQKVMRECGKPMILSSNRLYKWI 359
OY	356 PONDILGHPKTKAFTTTHGCMNGIYAIAHYGVPMGVPIFGQOLDNIAMKAKAAVEINF 415
DB	360 PONDILGHPKTKAFTTTHGCMNGIYAIAHYGVPMGVPIFGQOLDNIAMKAKAAVEINF 419
OY	416 KTMSEDELLRALFTVITDTSYKENAMRLSRTHHDPVAKPLDRAVAFWIEFVARKHAKHLR 475
DB	420 KTMSEDELLRALFTVITDTSYKENAMRLSRTHHDPVAKPLDRAVAFWIEFVARKHAKHLR 479
OY	476 SAHDLTWFOHYSIDVIGFLLTCVATAIFLTKCEPESCQKFNKTRKEKE 527
DB	480 SAHDLTWFOHYSIDVIGFLLTCVATAIFLTKCEPESCQKFNKTRKEKE 531
RESULT 12	
ID	UDBA_HUMAN STANDARD; PRT; 528 AA.
AC	P36537;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	UDP-GLUCURONOSYLTTRANSFERASE 2B10 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
GN	(UDPGLT).
GN	UGT2B10.
OC	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RC	MEDLINE=93326164; PubMed=833863;
RA	Jin C.-J., Miners J.O., Lillywhite K.J., McKenzie P.I.,
RT	"cDNA cloning and expression of two new members of the human liver
RT	UDP-glucuronosyltransferase 2B subfamily.";
RL	Biochem. Biophys. Res. Commun. 194:496-503(1993).
CC	-1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC	SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC	ENDOGENOUS COMPOUNDS.
CC	-1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC	BETA-D-GLUCURONOSIDE.
CC	-1- SUBCELLULAR LOCATION: MICROSOMAL.
CC	-1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTTRANSFERASE FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X63359; CAA44961.1; -
DR	PIR; JN0620; JN0620.
DR	MIM; 600070; -
DR	InterPro: IPR002213; -
DR	Pfam; PF00201; UDPGT; 1.
DR	PROSITE; PS00375; UDPGT; 1.
KW	Transferase; Glycosyltransferase; glycoprotein; Transmembrane; Signal;
KW	Multigene family; Microsome.
FT	SIGNAL 1 23
FT	CHAIN 1 23
FT	TRANSKEM 24 528
FT	CARBOHYD 492 512
FT	CARBOHYD 66 66
FT	CARBOHYD 314 314
FT	CARBOHYD 481 481
SEQUENCE	528 AA; 60774 MW; 56BEA3DBC032C2E0 CRC64;

Matches	311:	Conservative	72:	Mismatches	134:	Indels	3:	Gaps
QY	11	LLQL-FCVCGCGGAYVPCDMSHWLVKYLEELVHGHEVYVLTSHKPSLIDYRKP	69					
Db	9	LLQLSFYSSGSGGAYVAAEYSLMMNMKLTLLKLELVYRGHEVYVLTSSASITLFPDND	68					
QY	70	SAKFEVYVHPORTEENEIEFYDLA-LNVLPGLSTWQSVIKLNDFFVIRIGLTKMCS	127					
Db	69	STLKEVYVTSLTKEFEENIMQLYKRSLSELOKDTWLPFSSQDELMAINDIIRNFKD	128					
QY	128	EYVYVLTAKKLOETNYDVMIDPVIPOGDLMAELLAVPVLTLRLISVGNMERSCGLPA	187					
Db	129	VYSNMKLMKLDSESRDIEFADAYIPCGELLALFENIPVYSHSFSPGSFERSGGFIE	188					
QY	188	PLSYVVPMTGLDRTFELRYKNSMLSTLPHFWIODYHHMEERYSKALRPTLTCT	247					
Db	189	PSYVYVWVSKSLSDQMTFEYRYKNNLYLIEFPWQIFPMKKWDQPSVILRPTTLST	248					
QY	248	VGKAELIWLRTYWDPEEPQYQPNPEVVGGLHCKPAKAPKEMENFVSSGEGJYVST	307					
Db	249	MKRADILMRNSWNEKPEPFLPNVDVFGGLHCKPAKAPKMEERYVSSGEGVYVSTL	308					
QY	308	GSLFQVWTEKKNIIASAAQIPQVLYRKYKKKSTTGANTRLYDWIRPONDLCHEPKTK	367					
Db	309	GSMVSMTEERANVATATLAKIPQVLYMRFDGNKPDALGRLNRLKWIPONDLGHPKTR	368					
QY	368	AEITHGNGIYEALYHGVPVGVPIFGQDNIIMHAKAGAAYEINRTMSEDLAL	427					
Db	369	AEITHGAGNGIYEALYHGIPVGIPLFEDQPNIMHAKAGAAYVDPRTMSTLLNAL	428					
QY	428	RVIYVDSYKKNAMLSRIHQDPKPLDRAVFWLIEFYVRHKGAKHLRSAHDLTWFOHY	487					
Db	429	KVIYVDSYKKNAMLSRIHQDPKPLDRAVFWLIEFYVRHKGAKHLRVAAHNLTWFOYH	488					
QY	488	SIDVIGFLITCVATAIPLFTKCFLESCQKFNKTRIEKRE	527					
Db	489	SIDVIGFLITCVATVILFTKCCFLCFMKFPAKKGKGRD	528					
RESULT 13								
QY	1	UDBB_HUMAN	STANDARD;	PRT;	529	AA.		
Db	1	UDBB_HUMAN	STANDARD;	PRT;	529	AA.		
QY	AC	075310:						
Db	AC	075310:						
QY	DT	15-DEC-1998 (Rel. 37, Created)						
Db	DT	15-DEC-1998 (Rel. 37, Last sequence update)						
QY	DT	15-DEC-1998 (Rel. 37, Last annotation update)						
Db	DT	15-DEC-1998 (Rel. 37, Last annotation update)						
QY	DE	UDP-GLUCUCONOSYLTRANSFERASE ZB1 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPgt).						
Db	DE	UDP-GLUCUCONOSYLTRANSFERASE ZB1 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPgt).						
QY	GN	UGT2B11.						
Db	GN	UGT2B11.						
QY	OS	Homo sapiens (Human).						
Db	OS	Homo sapiens (Human).						
QY	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Db	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
QY	OX	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
Db	OX	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
QY	RN	NCBI_TaxID=9606;						
Db	RN	NCBI_TaxID=9606;						
QY	RX	[1]						
Db	RX	[1]						
QY	RX	SEQUENCE FROM N.A.						
Db	RX	SEQUENCE FROM N.A.						
QY	RA	MEDLINE=98340847; Pubmed=9675083;						
Db	RA	MEDLINE=98340847; Pubmed=9675083;						
QY	RT	Beaulieu M., Levesque E., Hum D.W., Belanger A.;						
Db	RT	Beaulieu M., Levesque E., Hum D.W., Belanger A.;						
QY	RT	"Isolation and characterization of a human orphan UDP-						
Db	RT	"Isolation and characterization of a human orphan UDP-						
QY	RL	glucuronosyltransferase, ugt2b11.";						

CC	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF016492; AAC27891.1; -
DR	MIM; 603064; -
DR	InterPro; IPRO02123; -
DR	Pfam; PF00201; UDBPGT: 1.
DR	PROSITE; PS00375; UDBPGT: 1.
KM	Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal; Multigene family; Microsome.
KW	SIGNAL
FT	CHAIN 1 21 POTENTIAL.
FT	CHAIN 22 529 UDBPGT.
FT	TRANSMEM 433 513 UDBPGT.
FT	CARBOHYD 315 315 N-LINKED (GLUCANAC. . .) (POTENTIAL).
SO	SEQUENCE 529 AA; 61038 MW; CEFA3C371CFC2AB4 CRC64;
Query Match	58.1%; Score 1628.5; DB 1; Length 529;
Best Local Similarity	58.9%; Pred. No. 5e-121;
Matches 312; Conservative 71; Mismatches 128; Indels 19; Gaps 4;	
QY	9 VELLIDLC-VCCGCGKVLVPCMSHWLVKYLEELIVRGHEVYLTGSKPSLIDYR 67
DB	8 VELLIDLCVCFSSGSGKVLVMAEYSWMNMKLTIKELVGRHEVYLVASSASILRDPN 67
QY	68 KPSALKEFEVHVPMDPTRENEIFVLDALNVLGSTWQSYVKLNDFFV-----EI 117
DB	68 DASLKEFEVYPPSLTKTEENI-----IMQVAKRW-SDIRKDSFWLVSQEDLILML 119
QY	118 RGTLLKMCESFIYNOTLKKILOETNYDVALIDPVLPGCDLMAELLAVFVLTIRISVGN 177
DB	120 YDIFRNFCKDQVYSNKKVMKKILOESRFIDVPADAVPCGELLALNIRFVYSLRFTPGYT 179
QY	178 MERSGCKLPAPISYVPVMTGLTDMETLEYSKMSLVLFHEHIOQDYDHFMEFYSKA 237
DB	180 IRRHSGGLTFPSTYIPYMSKLSIDQMTMERKNNIYLYLFDMPFQSDMKKMQDFSEV 239
QY	238 IGRPTTLCEYGAIAWILIRTYWDFEPQOPQPNFEFYGHLGCRAPALPKEMENFQSS 297
DB	240 IGRPTTLFETMGKADIMLRNMSMSQRPRLPVPNDVPGFGRHCKRPARLPKREMEFQSS 299
QY	298 GBDGIVYISLGLPQNVYEEKANIIASLADIPQVLMRKKGKPSYLGANTRLYDIPQ 357
DB	300 GENGVAVFSLGSVYSNMFAERANVATLAKIPQVLMRFDGKNRDLGINTRLYKIPQ 359
QY	358 NDLGHPRTKAFITGCGANGIYEALIHCVPWGVPIFGDOLDNIAHKKAGAVNEIKT 417
DB	360 NDLGHPRTKAFITGCGANGIYEALIHCVPWGVPIFGDOLDNIAHKKAGAVNEIKT 419
QY	418 MTSDDLRLALRTVITDSSYKENAMRLSRHHQDVPKDLRAVWIEFVMMRKKAKHLRSA 477
DB	420 MTSDDLRLALRTVINDPLYKENIMKLSIQHDQVPRDLRAVWIEFVMMRKKAKHLRSA 479
QY	478 AHDLMFPHYSIDVIGELTCVATATLELFCGLFSQCKNKRKRIEKE 527
DB	480 AHDLMFPHYSIDVIGELTCVATATVITLTKFLCFCWKKRKGKKRGK 529
RESULT 14	
UDCL_RABIT	
ID	UDCL_RABIT STANDARD; PRT; 502 AA.
AC	P36514;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	UDP-GUCCORONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17) (UDBPGT) (FRAGMENT).
GN	UGR221 OR UGR22A2.
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
NCBI	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
3X	NCBI_TaxID=9986;

KW Multigene family; Microsome.
FT SIGNAL 1 23
FT CHAIN 24 530
FT TRANSMEM 494 510
FT CARBOHYD 316 316
FT VARIANT 2 2
FT VARIANT 61 61
FT VARIANT 71 71
FT VARIANT 95 95
FT VARIANT 183 183
FT VARIANT 346 346
FT VARIANT 398 398
FT VARIANT 414 415
FT VARIANT 433 433
FT VARIANT 475 475
FT VARIANT 488 488
SQ SEQUENCE 530 AA, 61060 MW, D49313CE3B6D5BFD CRC64;
UPD-GLUCURONOSYLTRANSFERASE 2B12.
POTENTIAL.
N-LINKED (GLCNAC, . .) (POTENTIAL).
S -> P (IN KIDNEY).
F -> S (IN KIDNEY).
D -> H (IN KIDNEY).
N -> S (IN KIDNEY).
O -> K (IN KIDNEY).
P -> T (IN KIDNEY).
A -> G (IN KIDNEY).
VE -> AT (IN KIDNEY).
V -> D (IN KIDNEY).
K -> L (IN KIDNEY).
Q -> L (IN KIDNEY).

Query Match 56.9%; Score 1595; DB 1; Length 530;
Best Local Similarity 57.9%; Pred. No. 2,2e-118;
Matches 307; Conservative 74; Mismatches 143; Indels 6; Gaps 3;

OY 3 SDKSALVELLIDL-FCVGGCGKVLVWPCDMSHLNVKVLLEELIVRGHEVTLTHSKP 61
DB 2 SKRWISALLDQISFCFKSGCKGKVLWPMEXSHWNKIKIILEELVQKHGEVTLRPSAF 61
OY 62 SLIDYKPSALKFEVYVHMPODRENEIEFVDLALNV---LPGLSTWQSVIKLNDFFVEI 117
DB 62 VLDPRKETSCLKF-VTFPTSFSSHDLENFTFVNVWYELPRDCLSTFLYIQTIDEX 120
OY 118 RGTLMKMCESFYIYNOTLMAKLOETNYDWMLIDVIPCGLDLMALLAVPVLTLRISVGN 177
DB 121 SDYCLTVCKEAVSNQFMKIQESKDFVFSDAISGCGELIALLQIPFLYSIRFSPGYT 180
OY 178 MERSCGKLPAPLSYVPVPTGLDRTFLERYKNSMLSVLFHWIODYDHHMEEFYSKA 237
DB 181 IQOYIGVLFPPSYVPMIFSGLAGOMFTIERVHNMICMLYDFWFQTRKKWDPPYSKT 240
OY 238 LGRPTTLETVGKAEIWLIRTYWDEFEPQPYQPNFEVQGLHCKPAKALPKMENFVQSS 297
DB 241 LGRPTTLETVGKAEIWLIRTYWDEFEPQPYQPNFEVQGLHCKPAKALPKMENFVQSS 300
OY 298 GEDGIVFSLGSLFQNVTEERKANIISALAOIPQKVLWRKYKKRSTIGANTRLDWDIPQ 357
DB 301 GEHGVVFSLSGMVANNTEERKANIISALAOIPQKVLWRKYKKRSTIGANTRLDWDIPQ 360
OY 358 NDLLGHPRTKAFITHGANGIYEALYHGVPMWGPVIFGDOLDNIAMKAKGAAYEINFRT 417
DB 361 NDLLGHPRTKAFITHGANGIYEALYHGVPMWGPVIFGDOLDNIAMKAKGAAYEINFRT 420
OY 418 MTSDDLALRTVITLTDSSYKENAMRLSRHHDPYKPLDRAVFWTEFVWRHKGAKHLRSA 477
DB 421 MTKSDLLALAEVINDNPKYKNNAMWLSIHHDPYKPLDRAVFWTEFVWRHKGAKHLRSL 480
OY 478 AHDLTWFOHYSIDVIGFLTCVATAIFLTKCFLPSCKPFNKTRIEKRE 527
DB 481 GHNLPWYQYHSLDVIGFLSLCAVATVVALKCFLEFVYRFYKKEKKTKNE 530

Search completed: August 13, 2001, 13:43:02
Job time: 537 sec